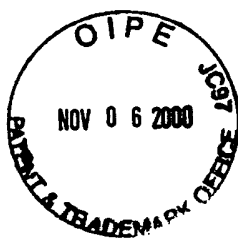


SEQUENCE LISTING



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<110> Fujii, Ryo
<110> Matsumoto, Hirokazu
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<150> JP 9-165437
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35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Pro Gly Asp Gly Pro
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Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
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Gln Glu

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TGGTACGCRG GCCGTGGGAT CCGGCCCGTG GGCCGCTTCG GCCGGCGAAG AGCTGCCCYG 180
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<213> Bovine

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<213> Bovine

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20 25 30

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33

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<213> Bovine

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Val Gly Arg Phe
20

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<211> 21

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<213> Bovine

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Val Gly Arg Phe Gly
20

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<211> 22

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<213> Bovine

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Val Gly Arg Phe Gly Arg
20

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<211> 87

<212> DNA

<213> Bovine

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GCRGGCCGTG GGATCCGGCC CGTGGGC 87

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<213> Bovine

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<211> 63

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<213> Bovine

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<211> 66

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<213> Bovine

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 Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
 35 40 45
 Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
 50 55 60
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
 65 70 75 80
 Val Val Leu Val His Pro Leu Arg Arg Arg Ile
 85 90

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 <212> PRT
 <213> Human
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 1 5 10 15
 Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
 20 25 30
 Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg
 35 40 45
 Thr Phe Cys Leu Leu Val Val Val Val Val Val
 50 55

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 <212> PRT
 <213> Human
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 20 25 30
 Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
 35 40 45
 Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
 50 55 60
 Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu
 65 70 75 80
 Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn

130 135 140
Tyr Ala Trp Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145 150 155 160
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165 170 175
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
180 185 190
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
195 200 205

<210> 23

<211> 126

<212> PRT

<213> Murine

<400> 23

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20 25 30
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
35 40 45
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile
50 55 60
Tyr Ala Trp Gly Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala
65 70 75 80
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
85 90 95
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
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<211> 273

<212> DNA

<213> Human

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GCCTTCGAGC CACGCGGCTG GGTGTTTCGGC GCGCGCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGGTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATC 273

<210> 25

<211> 177

<212> DNA

<213> Human

<400> 25

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GTGTCACTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC 120
TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG 177

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<211> 1110

<212> DNA

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GGCGCGGACG CTCACGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180
GGGCTGATCG TGCTGCTCTA CACCGTCGTG GTGGTTCGTG GGCTGGTGGG CAACTGCCTG 240
CTGGTGCTGG TGATCGCGCG GGTCCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC 300
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360
GCCTTCGAGC CACGCGGCTG GGTGTTCCGG GGCGGCCCTGT GCCACCTGGT CTTCTTCCTG 420
CAGCCGGTCA CCGTCTATGT GTCGGTCTTC ACGCTCACCA CCATCGCAGT GGACCGCTAC 480
GTCGTGCTGG TGCACCCGCT GAGGCGGCC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 540
CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 600
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 660
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 720
ATCCTCCTGT CTTACGTCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 840
GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGGTGCCCG TGCACGTCTT CAACCTGCTG 900
CGGGACCTCG ACCCCACGCG CATCGACCTT TACGCTTTTG GGCTGGTGCA GCTGCTCTGC 960
CACTGGCTCG CCATGAGTTC GGCTGCTAC AACCCTTCA TCTACGCCTG GCTGCACGAC 1020
AGCTTCCGCG AGGAGCTGCG CAACTGTTG GTCGCTTTCG CCCGCAAGAT AGCCCCCAT 1080
GGCCAGAATA TGACCGTCAG CGTGCTCATC 1110

<210> 27

<211> 618

<212> DNA

<213> Murine

<400> 27

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GCCTTCGAGC CACGCGGCTG GGTGTTCCGG GGCGGCCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGGCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGCTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 300
CTGGCCATCT GGGTGTGCTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 360
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 420
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 480
ATCCTCCTGT CTTACGCCCC GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCGCG 540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 600
GTGGTGGTCG TGGTGGTG 618

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<211> 378

<212> DNA

<213> Murine

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GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC 240
ATCCTCCTGT CTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC 300
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<211> 25

<212> DNA

<213> Unknown

<220>

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<212> DNA

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<211> 27

<212> DNA

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<223> Unsure

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<210> 32

<211> 29

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<210> 33

<211> 24

<212> DNA

<213> Unknown

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<223> Unsure

<400> 33

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<212> DNA

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<220>

<223> Unsure

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AACACCGACA CATAGACGGT GACC 24

<210> 35

<211> 20

<212> DNA

<213> Unknown

<220>

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C11

<223> Unsure

<400> 35

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<210> 36

<211> 26

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<213> Unknown

<220>

<223> Unsure

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<210> 37

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<212> DNA

<213> Unknown

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<210> 38

<211> 20

<212> DNA

<213> Unknown

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<400> 38

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<210> 39

<211> 28

<212> DNA

<213> Unknown

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<400> 39

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<210> 40

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 40

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<210> 41

<211> 27

<212> DNA

<213> Unknown

<220>

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<210> 42

<211> 32

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 42

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<213> Unknown
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<213> Bovine
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20 25 30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro
50 55 60
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
65 70 75 80
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
85 90 95
Gln Glu

<210> 45
<211> 83
<212> PRT
<213> Rat
<400> 45

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Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg
20 25 30
Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
35 40 45
Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly
50 55 60
Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser
65 70 75 80
Gln Arg Gly

<210> 46

<211> 249

<212> DNA

<213> Rat

<400> 46

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TACACGGGCC GCGGGATCAG GCCTGTGGGC CGCTTCGGCA GGAGAAGGGC AACCCCGAGG 180
GATGTCACTG GACTTGCCCA ACTCAGCTGC CTCCCACTGG ATGGACGCAC CAAGTTCTCT 240
CAGCGTGGA 249

<210> 47

<211> 31

<212> PRT

<213> Rat

<400> 47

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20 25 30

<210> 48

<211> 32

<212> PRT

<213> Rat

<400> 48

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
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Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

<210> 49

<211> 33

<212> PRT

<213> Rat

<400> 49

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Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly

Arg 20 25 30

<210> 50

<211> 20

<212> PRT

<213> Rat

<400> 50

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe
 20

<210> 51

<211> 21

<212> PRT

<213> Rat

<400> 51

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
 1 5 10 15
 Val Gly Arg Phe Gly
 20

*Sub
B1
Cm-k*

<210> 52

<211> 22

<212> PRT

<213> Rat

<400> 52

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
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 Val Gly Arg Phe Gly Arg
 20

<210> 53

<211> 93

<212> DNA

<213> Rat

<400> 53

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ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTC

93

<210> 54

<211> 96

<212> DNA

<213> Rat

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ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGC 96

<210> 55

<211> 99

<212> DNA

<213> Rat

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ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGCAGG 99

<210> 56

<211> 60

<212> DNA

<213> Rat

<400> 56

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<210> 57

<211> 63

<212> DNA

<213> Rat

<400> 57

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GGC 63

<210> 58

<211> 66

<212> DNA

<213> Rat

<400> 58

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GGCAGG 66

<210> 59

<211> 87

<212> PRT

<213> Human

<400> 59

Met Lys Val Leu Arg Ala Trp Leu Leu Cys Leu Leu Met Leu Gly Leu
1 5 10 15
Ala Leu Arg Gly Ala Ala Ser Arg Thr His Arg His Ser Met Glu Ile
20 25 30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg
35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Leu Gly Asp Val Pro
50 55 60
Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly
65 70 75 80
Ala Met Ser Ser Gln Asp Gly
85

<210> 60

<211> 261

<212> DNA

<213> Human

<400> 60

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TGGTACGCCA GTCGCGGGAT CAGGCCTGTG GGCCGCTTCG GTCGGAGGAG GGCAACCCTG 180
GGGGACGTCC CCAAGCCTGG CCTGCGACCC CGGCTGACCT GCTTCCCCTT GGAAGGCGGT 240
GCTATGTCGT CCCAGGATGG C 261

<210> 61

<211> 31

<212> PRT

<213> Human

<400> 61

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1 5 10 15
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe

20

25

30

<210> 62

<211> 32

<212> PRT

<213> Human

<400> 62

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Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

<210> 63

<211> 33

<212> PRT

<213> Human

<400> 63

Ser	Arg	Thr	His	Arg	His	Ser	Met	Glu	Ile	Arg	Thr	Pro	Asp	Ile	Asn
1				5					10					15	
Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro	Val	Gly	Arg	Phe	Gly
			20					25					30		

Arg

<210> 64

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<212> PRT

<213> Human

<400> 64

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1				5					10					15	
Val	Gly	Arg	Phe												
			20												

<210> 65

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<400> 65

Thr	Pro	Asp	Ile	Asn	Pro	Ala	Trp	Tyr	Ala	Ser	Arg	Gly	Ile	Arg	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1 5
Val Gly Arg Phe Gly
20

10

15

<210> 66

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1 5 10 15
Val Gly Arg Phe Gly Arg
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<210> 67

<211> 93

<212> DNA

<213> Human

<400> 67

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<210> 68

<211> 96

<212> DNA

<213> Human

<400> 68

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<210> 69

<211> 99

<212> DNA

<213> Human

<400> 69

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<210> 70

<211> 60

<212> DNA

<213> Human

<400> 70

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<210> 71

<211> 63

<212> DNA

<213> Human

<400> 71

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GGT 63

<210> 72

<211> 66

<212> DNA

<213> Human

<400> 72

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<210> 73

<211> 21

<212> PRT

<213> Unknown

<220>

<223> Unsure. Xaa of the 10th position is Ala or Thr.
Xaa of the 11th position is Gly or Ser.
Xaa of the 21st position is H, Gly or GlyArg.

<400> 73

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Xaa Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Xaa
20

<210> 74

<211> 11

<212> PRT

<213> Unknown

<220>

<223> Unsure. Xaa of the 3rd position is Ala or Thr.
Xaa of the 5th position is Gln or Arg.
Xaa of the 10th position is Ile or Thr.

<400> 74

Ser	Arg	Xaa	His	Xaa	His	Ser	Met	Glu	Xaa	Arg
1				5					10	

<210> 75

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 75

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<210> 76

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 76

TACCAGGCAG GATTGATACA GGGG 24

<210> 77

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 77

GGCATCATCC AGGAAGACGG AGCAT 25

<210> 78

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 78

AGCAGAGGAG AGGGAGGGTA GAGGA 25

<210> 79

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 79

ACGTGGCTTC TGTGCTTGCT GC 22

<210> 80

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

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GCCTGATCCC GCGGCCCGTG TACCA 25

<210> 81

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

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TTGCCCTTCT CCTGCCCAAG CGGCCC 26

<210> 82

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

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GGCGGGGGCT GCAAGTCGTA CCCATCG 27

<210> 83

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<212> DNA

<213> Unknown

<220>

<223> Unsure

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CGGCACTCCA TGGAGATCCG CACCCCT 27

<210> 84

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

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CAGGCAGGAT TGATGTCAGG GGTGCGG 27

<210> 85

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<212> DNA

<213> Unknown

<220>

<223> Unsure

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CATGGAGTGC CGATGGGTAC GACTTGC 27

<210> 86

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 86

GGCCTCCTCG GAGGAGCCAA GGGATGA 27

<210> 87

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 87

GGGAAAGGAG CCCGAAGGAG AGGAGAG 27

<210> 88

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 88

CCTGCTGGCC ATTCTCCTGT CTTAC 25

<210> 89

<211> 25

<212> DNA

<213> Unknown

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<223> Unsure

<400> 89

GGGTCCAGGT CCCGCAGAAG GTTGA 25

<210> 90

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 90

GAAGACGGAG CATGGCCCTG AAGAC 25

<210> 91

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 91

GGCAGCTGAG TTGGCCAAGT CCAGT 25

<210> 92

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 92

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Cys
1 5 10 15

<210> 93

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 93

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
1 5 10 15

<210> 94

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 94

Cys Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly
1 5 10 15

<210> 95

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 95

AGATTGGCAT CATCCAGGAA GACGGAGCAT 30

<210> 96

<211> 31

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 96

GCTGACTCGA CAGCACTGTC TTCTCGAGCT G 31

<210> 97

<211> 21

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 97

AACCCCTTCA TCTATGCGTG G 21

<210> 98

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 98

ATATTCTGGC CATGAGGCAC 20

<210> 99

<211> 28

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 99

TTCCGAGAGG AGCTACGCAA GATGCTTC 28

Ans
B1
nk
